

Figure 1

Position number	Sequence	Position	2D6 (IgM)	4B6 (IgG <sub>1</sub> )	5C6 (IgG <sub>2a</sub> )	6D7 (IgG <sub>1</sub> )
6	EKDGLRNSTGLGSQN	26-40				
7	RNSTGLGSQNKFFVVG	31-45				
29	QCSTIGQMPNNQSIN	141-155				
30	GQMPNNQSINSKVSQ	146-160				
36	SEVSGTQKVSFSGQP	176-190				
37	TQKVSFSGQPQNITT	181-195				
77	GKTFITNGWKSTEEED	381-395				
87	EKGTGESQSRDRRKI	431-445				
88	ESQSRDRRKIDQHTL	436-450				
92	NRTDLDPRVLSNSGW	456-470				
93	DPRVLSNSGWGQTPI	461-475				
105	GNDTSSVSGWGDPKP	521-535				
106	SVSGWGDPPKALRWG	526-540				
109	DSKGSNCQGGWEDDS	541-555				
117	KNKQGWGDGQKSSQG	581-595				
118	WGDGQKSSQGWVSVA	586-600				
119	KSSQGWVSASDNWG	591-605				
125	SSGGSDSDRSVSGWN	621-635				
126	DSDRSVSGWNLGKT	626-640				
127	VSGWNLGKTSSFTW	631-645				
130	GNNINPNSSGWDES	646-660				
133	SKPTPSQGWGDPPKS	661-675				
134	SQGWGDPPKSNQSLG	666-680				
135	DPPKSNQSLGWGDSS	671-685				
136	NQSLGWGDSSKPVSS	676-690				
137	WGDSSKPVSSPDWVK	681-695				
138	KPVSSPDWVKQQDIV	686-700				
139	PDWVKQQDIVGSWGI	691-705				
146	AKEEPTGWEEPSPE	726-740				
150	MEIDDGTSAWGDPSK	746-760				
154	VNMWVNKNVPNGNSRS	766-780				
159	TPASAINKEASSGS	791-805				
160	ISNKEASSGSGWGEF	796-810				
161	ASSGSGWGEFWEPS	801-815				
162	GWGEFWEFSTPATT	806-820				
176	DDMPLPGNRPTGWEE	876-890				
177	PGNRPTGWEEEDVE	881-895				
178	TGWEEEDVEIGNWN	886-900				
185	SSKGLSGKKRRRERG	921-935				
187	RRERGMMKGGNKQEE	931-945				
191	FVKQFSNISFSRDSF	951-965				
192	SNISFSRDSPEENVQ	956-970				
198	MEIDKHSNLNIGDYNR	986-1000				
199	HSLNIGDYNRTVGKG	991-1005				
200	FGYNRTVGKGPGSRP	996-1010				
201	TVGKGPGSRPQISKE	1001-1015				
202	PGSRPQISKESMER	1006-1020				
203	QISKESMERNPYFD	1011-1025				
221	PLSSSQPNLRAQVPP	1101-1115				
226	LLKYAPNNGGLNPLF	1126-1140				
227	PNNGGLNPLFGPQQV	1131-1145				
228	LNPLFGPQQVAMLNQ	1136-1150				
233	SQLQRLLAQQRAS	1161-1175				
234	LLAQQRASQSRVP	1166-1180				
235	QRAQSRVPSQNR	1171-1185				
239	GRPLSVQQMMQQR	1191-1205				
270	SPNGSSVNWPFEPF	1346-1360				
271	SSVNWPFEPFGEF	1351-1365				
274	KGYPNIDPETDPYVT	1366-1380				
276	KPYVTPGVSINNLSI	1376-1390				
287	PLSSTAQSTSARNSD	1431-1445				
288	AQSTSARNSDSKLTW	1436-1450				
298	GQKPLSTWDNSPLR	1486-1500				
299	LSTWDNSPLRIGGGW	1491-1505				
304	SSWGESSSGRITNWL	1516-1530				
319	TTILAEFASSEEISR	1591-1605				
320	EFASSEEISRFFAQS	1596-1610				
323	QSLTPSPGWQSLGSS	1611-1625				
324	SPGWQSLGSSQSR	1616-1630				
336	WGPPSSSDPRGISSP	1676-1690				
339	SPINAFSLVDHLGGG	1691-1705				
340	AFLSVVDHLGGGGESM	1696-1710				



Figure 2

PEPTIDE			PATIENT		
Number	Sequence	Position	#1	#3	#10
6	EKDGLRNSTGLGSON	26-40			
7	RNSTGLGSONKFVVG	31-45			
18	NNRMNAWGTVSSSSN	86-100			
22	STLNSASNHGAWPVL	106-120			
29	QCSTIGQMPNNQSN	141-155			
30	GQMPNNQSNKVSQ	146-160			
36	SEVSOTOKVSFSQOP	176-190			
37	TOKVSFSQOPONITT	181-195			
45	ELPSSNTQAWRVSTM	221-235			
34	GTTWQAGYGSNYSQDK	266-280			
55	AYGSNYSQDKCSGPN	271-285			
63	QVNTNKGQGVWESGA	311-325			
64	KGGGVWESGAANSQS	316-330			
65	WESGAANSQSTSWSGS	321-335			
67	TSWQSGNQANSQSSR	331-345			
68	GNGANSQSGRRGWGT	336-350			
77	GKTFINGWKSTEEED	381-395			
78	NGWKSTEEEDQGSAT	386-400			
87	EKGTGESQSRDRRKI	431-445			
88	ESQSRDRRKIDQHTL	436-450			
92	NRTDLDPVLSNSGW	456-470			
93	DPRVLSNSGWQQTPI	461-475			
97	WDTETSPRGERKTDN	481-495			
105	GNDTSSVSGWDPFKP	521-535			
106	SVSGWGDPPKALRWG	526-540			
117	KNKQGWGDQKSSQSG	581-595			
118	WGDGQKSSQGSVSA	586-600			
133	SKPTPSQGWGDPKPS	661-675			
134	SQGWGDPPKSNQSLG	666-680			
135	DPPKSNQSLGWGDSS	671-685			
136	NQSLGWGDSSKPVSS	676-690			
137	WGDSSKPVSSPDWKN	681-695			
138	KPVSSPDWKNQQDIV	686-700			
139	PDWKNQQDIVQSWG	691-705			
148	EPSSESIRRKMEIDD	736-750			
150	MEIDDTSAWGDPSK	746-760			
154	VNMWKNVPNGNSRS	766-780			
171	WGSSVQOPALSKSQ	851-865			
177	PCNRRPTGWEEEDVE	881-895			
185	SSKGLSKKKRRRERG	921-935			
187	RRERQMMKGGQKQEE	931-945			
189	NKQEEAWINPFVKQF	941-955			
190	AWINPFVKQFSNISF	946-960			

191	FVKQFSNISFSRDS	951-965			
192	SNISFSRDSPEENVQ	956-970			
198	MEIDKHSLNIGDYNR	986-1000			
199	HSLNIGDYNRVTGKG	991-1005			
200	GDYNRTVGKGPQSRP	996-1010			
201	TVGKGPQSRPQISKE	1001-1015			
202	PGSRPQISKESMER	1006-1020			
217	MFGVNTAAOPRGMQ	1081-1095			
220	QPPAQPLSSSQPNLR	1096-1110			
221	PLSSSQPNLRAQVPP	1101-1115			
227	PNNGLNPLFGPQQV	1131-1145			
228	LNPLFGPQQVAMLNQ	1136-1150			
231	LSQLNQLSQISQLQR	1151-1165			
233	SQLQRLLAQQQRAQS	1161-1175			
234	LLAQQRAQSQRSVP	1166-1180			
235	QRAQSQRSVPSGNRP	1171-1185			
239	GRPLSVQQQMMQQR	1191-1205			
256	KEPQSRRLKWTTVDS	1276-1290			
257	RLRKWTTVDSISVNT	1281-1295			
263	FRLEESFPVPYDFMN	1311-1325			
264	SPFVPYDFMNSSTSP	1316-1330			
270	SPNGSSSVNWPPEFR	1346-1360			
271	SSVNWPPEFRPQEPW	1351-1365			
272	PPEFRPQEPWKGYFN	1356-1370			
273	PQEPWKGYFNIDPET	1361-1375			
276	DPYVTPGSSVINLSI	1376-1390			
279	NTVREVDHLDRNSG	1391-1405			
280	VDHLDRNSGSSSSL	1396-1410			
287	PLSSTAQSTSARNSD	1431-1445			
288	AQSTSARNSDSKLTW	1436-1450			
292	TNTSLAHELWKVPLP	1456-1470			
293	AHELWKVPLPKNIT	1461-1475			
294	KVPLPKNITAPSRP	1466-1480			
297	PPGLTGQKPLSTWD	1481-1495			
298	GQKPLSTWDNSPLR	1486-1500			
300	NSPLRIGGGWONSDA	1496-1510			
301	IGGGWONSARYTPO	1501-1515			
302	QNSDARYTPGSSWGE	1506-1520			
303	RYTPGSSWGESSGR	1511-1525			
304	SSWGESSGRITNWL	1516-1530			
313	LPHGNALVRYSSKEE	1561-1575			
314	ALVRYSSKEEVVKAQ	1566-1580			
323	QSLTPSGWQSLGSS	1611-1625			
324	SPGWQSLGSSQSRIG	1616-1630			
335	YSTSLWGPPSSSDPR	1671-1685			
336	WGPPSSSDPRGISSP	1676-1690			
337	SSDPRGISSSPINA	1681-1695			
338	GISSSPINAFSLVD	1686-1700			
339	SPINAFSLVDHLGGG	1691-1705			
340	AFLSVDHLGGGGESM	1696-1710			